



003300-589.ST25

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## SEQUENCE LISTING

TECH CENTER 1600/2900

<110> ULF, Lindahl  
LI, Jin-Ping

<120> DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a  
Process for Its Production

<130> 003300-589

<140> US 09/403,269  
<141> 1999-10-18

<150> SE 9701454-2  
<151> 1997-04-18

<150> PCT/SE98/00703  
<151> 1998-04-17

<160> 13

<170> PatentIn version 3.0

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17

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<223> Amino acid 5 is Xaa wherein Xaa = any amino acid.

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Pro Asn Asp Trp Xaa Val Pro Lys Gly Cys Phe Met Ala  
1 5 10

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<222> (2)..(10)  
<223> Amino acids 2 and 10 are Xaa wherein Xaa = any amino acid.

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 1 5 10

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&lt;400&gt; 4

Pro Asn Asp Xaa Thr Val Pro Lys  
 1 5

<210> 5  
 <211> 15  
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 <222> (1)..(11)  
 <223> Amino acids 1, 2 and 11 are Xaa wherein Xaa = any amino acid.

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Xaa Xaa Ile Ala Pro Glu Thr Ser Glu Gly Xaa Ser Leu Gln Leu  
 1 5 10 15

<210> 6  
 <211> 10  
 <212> PRT  
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&lt;400&gt; 6

Gly Gly Trp Pro Ile Met Val Thr Arg Lys  
 1 5 10

<210> 7  
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 <212> PRT  
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&lt;400&gt; 7

Phe Leu Ser Glu Gln His Gly Val  
 1 5

<210> 8  
 <211> 36

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<222> (30)..(30)  
<223> Amino acid 30 is Xaa wherein Xaa = any amino acid.

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Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile Tyr Asp  
1 5 10 15

Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Xaa Trp Asp  
20 25 30

Tyr His Thr Thr  
35

<210> 9<211> 25<212> DNA<213> Human<220><221> misc\_feature<222>  
(14)..(23)<223> Nucleotides 14, 20 and 23 are "n" wherein "n" = any  
nucleotide.

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25

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26

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          Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg

gtc aag tgc ata agt ggg gtt gaa ggt gta cct tta tct aca cag tgg      159
Val Lys Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp
          15      20      25

gga cct caa ggc tat ttc tac cca atc cag att gca cag tat ggg tta      207
Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu
          30      35      40      45

agt cac tac agc aag aat cta act gaa aaa ccc cct cat ata gag gta      255
Ser His Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val
          50      55      60

tat gaa aca gca gaa gac agg gac aaa aac agc aag ccc aat gac tgg      303
Tyr Glu Thr Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp
          65      70      75

act gtg ccc aag ggc tgc ttt atg gct agt gtg gct gat aag tca aga      351
Thr Val Pro Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg
          80      85      90

ttc acc aat gtt aaa cag ttc att gct cca gaa acc agt gaa ggt gta      399
Phe Thr Asn Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val
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tcc ttg caa ctg ggg aac aca aaa gat ttt att att tca ttt gac ctc      447
Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu
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Lys Phe Leu Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu
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Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile
          145      150      155

gct ttt aaa gaa aga gac ata tac tat ggc atc ggg ccc aga aca tca      591
Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser
          160      165      170

tgg agc aca gtt acc cgg gac ctg gtc act gac ctc agg aaa gga gtg      639
Trp Ser Thr Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val
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acc atc tct acc aca gcc cac atg gct gcc ttc ttc gct gcc agt gac Thr Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp 225 230 235	783
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acc cgt aag tta ggg gaa ggc ttc aag tct tta gag cca ggg tgg tac Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr 255 260 265	879
tcc gcc atg gcc caa ggg caa gcc att tct aca tta gtc agg gcc tat Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr 270 275 280 285	927
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gag cgt ggc atg gaa tcc ctt aaa gcc atg ctc ccc ttg tac gac act Glu Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr 370 375 380	1215
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ccc aac ctg gcc cgc tgg gac tat cac acc acc cac atc aat caa ctg Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu 400 405 410	1311
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Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val  
 415 420 425

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 Lys Arg Trp Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn  
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 35 40 45

Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr  
 50 55 60

Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp Thr Val Pro  
 65 70 75 80

Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Phe Thr Asn  
 85 90 95

Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln  
 100 105 110

Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Phe Leu  
 115 120 125

Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln  
 130 135 140

Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Lys  
 145 150 155 160

Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr

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Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser 180 185 190		
Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys Lys Val Val 195 200 205		
Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser 210 215 220		
Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val 225 230 235 240		
Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys 245 250 255		
Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met 260 265 270		
Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr 275 280 285		
Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr Ala Pro Tyr 290 295 300		
Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys 305 310 315 320		
His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu 325 330 335		
Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr 340 345 350		
Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly 355 360 365		
Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly 370 375 380		
Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu 385 390 395 400		



Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu  
 405 410 415

Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp  
 420 425 430

Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn  
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